SEQUENCE LISTING

<110> Davydova, Elena K.
Rothman-Denes, Lucia B.
Dahl, Gary A.
Gerdes, Svetlana Y.
Jendrisak, Jerome J.

<120> PREPARATION AND USE OF SINGLE-STRANDED TRANSCRIPTION SUBSTRATES
FOR SYNTHESIS OF TRANSCRIPTION PRODUCTS CORRESPONDING TO TARGET
SEQUENCES

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Ser His Ile Lys Val Thr Pro Leu Asp Ser Arg Leu Asn Ala Pro Ala
885 890 895

Ala Glu Val Val Lys Ala Phe Arg Gln Gly Asn Arg Asp Val Ala Ser
900 905 910

Ser Gln Pro Lys Ala Asp Ser Val Asn Gln Val Lys Glu Thr Pro Val
915 920 925

Thr Lys Gln Glu Pro Val Thr Ser Thr Val Gln Thr Lys Thr Pro Val
930 935 940

Ser Glu Ser Val Lys Thr Glu Pro Thr Thr Lys Glu Ser Ser Pro Gln

945 950 955 960

Ala Ile Lys Glu Pro Val Asn Gln Ser Glu Lys Gln Asp Val Asn Leu
965 970 975

Thr Asn Glu Asp Asn Ile Lys Gln Pro Thr Glu Ser Val Lys Glu Thr
980 985 990

Glu Thr Ser Thr Lys Glu Ser Thr Val Thr Glu Glu Leu Lys Glu Gly
995 1000 1005

Ile Asp Ala Val Tyr Pro Ser Leu Val Gly Thr Ala Asp Ser Lys Ala
1010 1015 1020

Glu Gly Ile Lys Asn Tyr Phe Lys Leu Ser Phe Thr Leu Pro Glu Glu
1025 1030 1035 1040

Gln Lys Ser Arg Thr Val Gly Ser Glu Ala Pro Leu Lys Asp Val Ala
1045 1050 1055

Gln Ala Leu Ser Ser Arg Ala Arg Tyr Glu Leu Phe Thr Glu Lys Glu
1060 1065 1070

Thr Ala Asn Pro Ala Phe Asn Gly Glu Val Ile Lys Arg Tyr Lys Glu
1075 1080 1085

Leu Met Glu His Gly Glu Gly Ile Ala Asp Ile Leu Arg Ser Arg Leu
1090 1095 1100

Ala Lys Phe Leu Asn Thr Lys Asp Val Gly Lys Arg Phe Ala Gln Gly
1105 1110 1115 1120

Thr Glu Ala Asn Arg Trp Val Gly Gly Lys Leu Leu Asn Ile Val Glu
1125 1130 1135

Gln Asp Gly Asp Thr Phe Lys Tyr Asn Glu Gln Leu Leu Gln Thr Ala
1140 1145 1150

Val Leu Ala Gly Leu Gln Trp Arg Leu Thr Ala Thr Ser Asn Thr Ala
1155 1160 1165

Ile Lys Asp Ala Lys Asp Val Ala Ala Ile Thr Gly Ile Asp Gln Ala
1170 1175 1180

Leu Leu Pro Glu Gly Leu Val Glu Gln Phe Asp Thr Gly Met Thr Leu
1185 1190 1195 1200

Thr Glu Ala Val Ser Ser Leu Ala Gln Lys Ile Glu Ser Tyr Trp Gly

1205 1210 1215

Leu Ser Arg Asn Pro Asn Ala Pro Leu Gly Tyr Thr Lys Gly Ile Pro
1220 1225 1230

Thr Ala Met Ala Ala Glu Ile Leu Ala Ala Phe Val Glu Ser Thr Asp
1235 1240 1245

Val Val Glu Asn Ile Val Asp Met Ser Glu Ile Asp Pro Asp Asn Lys
1250 1255 1260

Lys Thr Ile Gly Leu Tyr Thr Ile Thr Glu Leu Asp Ser Phe Asp Pro
1265 1270 1275 1280

Ile Asn Ser Phe Pro Thr Ala Ile Glu Glu Ala Val Leu Val Asn Pro
1285 1290 1295

Thr Glu Lys Met Phe Phe Gly Asp Asp Ile Pro Pro Val Ala Asn Thr
1300 1305 1310

Gln Leu Arg Asn Pro Ala Val Arg Asn Thr Pro Glu Gln Lys Ala Ala
1315 1320 1325

Leu Lys Ala Glu Gln Ala Thr Glu Phe Tyr Val His Thr Pro Met Val
1330 1335 1340

Gln Phe Tyr Glu Thr Leu Gly Lys Asp Arg Ile Leu Glu Leu Met Gly
1345 1350 1355 1360

Ala Gly Thr Leu Asn Lys Glu Leu Leu Asn Asp Asn His Ala Lys Ser
1365 1370 1375

Leu Glu Gly Lys Asn Arg Ser Val Glu Asp Ser Tyr Asn Gln Leu Phe
1380 1385 1390

Ser Val Ile Glu Gln Val Arg Ala Gln Ser Glu Asp Ile Ser Thr Val
1395 1400 1405

Pro Ile His Tyr Ala Tyr Asn Met Thr Arg Val Gly Arg Met Gln Met
1410 1415 1420

Leu Gly Lys Tyr Asn Pro Gln Ser Ala Lys Leu Val Arg Glu Ala Ile
1425 1430 1435 1440

Leu Pro Thr Lys Ala Thr Leu Asp Leu Ser Asn Gln Asn Asn Glu Asp
1445 1450 1455

Phe Ser Ala Phe Gln Leu Gly Leu Ala Gln Ala Leu Asp Ile Lys Val

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          1460                1465                1470

His Thr Met Thr Arg Glu Val Met Ser Asp Glu Leu Thr Lys Leu Leu
       1475                1480                1485

Glu Gly Asn Leu Lys Pro Ala Ile Asp Met Met Val Glu Phe Asn Thr
   1490                1495                1500

Thr Gly Ser Leu Pro Glu Asn Ala Val Asp Val Leu Asn Thr Ala Leu
1505                1510                1515                1520

Gly Asp Arg Lys Ser Phe Val Ala Leu Met Ala Leu Met Glu Tyr Ser
               1525                1530                1535

Arg Tyr Leu Val Ala Glu Asp Lys Ser Ala Phe Val Thr Pro Leu Tyr
          1540                1545                1550

Val Glu Ala Asp Gly Val Thr Asn Gly Pro Ile Asn Ala Met Met Leu
       1555                1560                1565

Met Thr Gly Gly Leu Phe Thr Pro Asp Trp Ile Arg Asn Ile Ala Lys
   1570                1575                1580

Gly Gly Leu Phe Ile Gly Ser Pro Asn Lys Thr Met Asn Glu His Arg
1585                1590                1595                1600

Ser Thr Ala Asp Asn Asn Asp Leu Tyr Gln Ala Ser Thr Asn Ala Leu
               1605                1610                1615

Met Glu Ser Leu Gly Lys Leu Arg Ser Asn Tyr Ala Ser Asn Met Pro
          1620                1625                1630

Ile Gln Ser Gln Ile Asp Ser Leu Leu Ser Leu Met Asp Leu Phe Leu
       1635                1640                1645

Pro Asp Ile Asn Leu Gly Glu Asn Gly Ala Leu Glu Leu Lys Arg Gly
   1650                1655                1660

Ile Ala Lys Asn Pro Leu Thr Ile Thr Ile Tyr Gly Ser Gly Ala Arg
1665                1670                1675                1680

Gly Ile Ala Gly Lys Leu Val Ser Ser Val Thr Asp Ala Ile Tyr Glu
               1685                1690                1695

Arg Met Ser Asp Val Leu Lys Ala Arg Ala Lys Asp Pro Asn Ile Ser
          1700                1705                1710

Ala Ala Met Ala Met Phe Gly Lys Gln Ala Ala Ser Glu Ala His Ala
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      1715                1720                1725

Glu Glu Leu Leu Ala Arg Phe Leu Lys Asp Met Glu Thr Leu Thr Ser
   1730                1735                1740

Thr Val Pro Val Lys Arg Lys Gly Val Leu Glu Leu Gln Ser Thr Gly
1745                1750                1755                1760

Thr Gly Ala Lys Gly Lys Ile Asn Pro Lys Thr Tyr Thr Ile Lys Gly
            1765                1770                1775

Glu Gln Leu Lys Ala Leu Gln Glu Asn Met Leu His Phe Phe Val Glu
          1780                1785                1790

Pro Leu Arg Asn Gly Ile Thr Gln Thr Val Gly Glu Ser Leu Val Tyr
       1795                1800                1805

Ser Thr Glu Gln Leu Gln Lys Ala Thr Gln Ile Gln Ser Val Val Leu
   1810                1815                1820

Glu Asp Met Phe Lys Gln Arg Val Gln Glu Lys Leu Ala Glu Lys Ala
1825                1830                1835                1840

Lys Asp Pro Thr Trp Lys Lys Gly Asp Phe Leu Thr Gln Lys Glu Leu
            1845                1850                1855

Asn Asp Ile Gln Ala Ser Leu Asn Asn Leu Ala Pro Met Ile Glu Thr
          1860                1865                1870

Gly Ser Gln Thr Phe Tyr Ile Ala Gly Ser Glu Asn Ala Glu Val Ala
       1875                1880                1885

Asn Gln Val Leu Ala Thr Asn Leu Asp Asp Arg Met Arg Val Pro Met
   1890                1895                1900

Ser Ile Tyr Ala Pro Ala Gln Ala Gly Val Ala Gly Ile Pro Phe Met
1905                1910                1915                1920

Thr Ile Gly Thr Gly Asp Gly Met Met Met Gln Thr Leu Ser Thr Met
            1925                1930                1935

Lys Gly Ala Pro Lys Asn Thr Leu Lys Ile Phe Asp Gly Met Asn Ile
          1940                1945                1950

Gly Leu Asn Asp Ile Thr Asp Ala Ser Arg Lys Ala Asn Glu Ala Val
       1955                1960                1965

Tyr Thr Ser Trp Gln Gly Asn Pro Ile Lys Asn Val Tyr Glu Ser Tyr
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1970 1975 1980

Ala Lys Phe Met Lys Asn Val Asp Phe Ser Lys Leu Ser Pro Glu Ala
1985 1990 1995 2000

Leu Glu Ala Ile Gly Lys Ser Ala Leu Glu Tyr Asp Gln Arg Glu Asn
2005 2010 2015

Ala Thr Val Asp Asp Ile Ala Asn Ala Ala Ser Leu Ile Glu Arg Asn
2020 2025 2030

Leu Arg Asn Ile Ala Leu Gly Val Asp Ile Arg His Lys Val Leu Asp
2035 2040 2045

Lys Val Asn Leu Ser Ile Asp Gln Met Ala Ala Val Gly Ala Pro Tyr
2050 2055 2060

Gln Asn Asn Gly Lys Ile Asp Leu Ser Asn Met Thr Pro Glu Gln Gln
2065 2070 2075 2080

Ala Asp Glu Leu Asn Lys Leu Phe Arg Glu Glu Leu Glu Ala Arg Lys
2085 2090 2095

Gln Lys Val Ala Lys Ala Arg Ala Glu Val Lys Glu Glu Thr Val Ser
2100 2105 2110

Glu Lys Glu Pro Val Asn Pro Asp Phe Gly Met Val Gly Arg Glu His
2115 2120 2125

Lys Ala Ser Gly Val Arg Ile Leu Ser Ala Thr Ala Ile Arg Asn Leu
2130 2135 2140

Ala Lys Ile Ser Asn Leu Pro Ser Thr Gln Ala Ala Thr Leu Ala Glu
2145 2150 2155 2160

Ile Gln Lys Ser Leu Ala Ala Lys Asp Tyr Lys Ile Ile Tyr Gly Thr
2165 2170 2175

Pro Thr Gln Val Ala Glu Tyr Ala Arg Gln Lys Asn Val Thr Glu Leu
2180 2185 2190

Thr Ser Gln Glu Met Glu Glu Ala Gln Ala Gly Asn Ile Tyr Gly Trp
2195 2200 2205

Thr Asn Phe Asp Asp Lys Thr Ile Tyr Leu Val Ser Pro Ser Met Glu
2210 2215 2220

Thr Leu Ile His Glu Leu Val His Ala Ser Thr Phe Glu Glu Val Tyr

2225 2230 2235 2240

Ser Phe Tyr Gln Gly Asn Glu Val Ser Pro Thr Ser Lys Gln Ala Ile
2245 2250 2255

Glu Asn Leu Glu Gly Leu Met Glu Gln Phe Arg Ser Leu Asp Ile Ser
2260 2265 2270

Lys Asp Ser Pro Glu Met Arg Glu Ala Tyr Ala Asp Ala Ile Ala Thr
2275 2280 2285

Ile Glu Gly His Leu Ser Asn Gly Phe Val Asp Pro Ala Ile Ser Lys
2290 2295 2300

Ala Ala Ala Leu Asn Glu Phe Met Ala Trp Gly Leu Ala Asn Arg Ala
2305 2310 2315 2320

Leu Ala Ala Lys Gln Lys Arg Thr Ser Ser Leu Val Gln Met Val Lys
2325 2330 2335

Asp Val Tyr Gln Ala Ile Lys Lys Leu Ile Trp Gly Arg Lys Gln Ala
2340 2345 2350

Pro Ala Leu Gly Glu Asp Met Phe Ser Asn Leu Leu Phe Asn Ser Ala
2355 2360 2365

Ile Leu Met Arg Ser Gln Pro Thr Thr Gln Ala Val Ala Lys Asp Gly
2370 2375 2380

Thr Leu Phe His Ser Lys Ala Tyr Gly Asn Asn Glu Arg Leu Ser Gln
2385 2390 2395 2400

Leu Asn Gln Thr Phe Asp Lys Leu Val Thr Asp Tyr Leu Arg Thr Asp
2405 2410 2415

Pro Val Thr Glu Val Glu Arg Arg Gly Asn Val Ala Asn Ala Leu Met
2420 2425 2430

Ser Ala Thr Arg Leu Val Arg Asp Val Gln Ser His Gly Phe Asn Met
2435 2440 2445

Thr Ala Gln Glu Gln Ser Val Phe Gln Met Val Thr Ala Ala Leu Ala
2450 2455 2460

Thr Glu Ala Ala Ile Asp Pro His Ala Met Ala Arg Ala Gln Glu Leu
2465 2470 2475 2480

Tyr Thr His Val Met Lys His Leu Thr Val Glu His Phe Met Ala Asp

2485 2490 2495

Pro Asp Ser Thr Asn Pro Ala Asp Arg Tyr Tyr Ala Gln Gln Lys Tyr
2500 2505 2510

Asp Thr Ile Ser Gly Ala Asn Leu Val Glu Val Asp Ala Lys Gly Arg
2515 2520 2525

Thr Ser Leu Leu Pro Thr Phe Leu Gly Leu Ala Met Val Asn Glu Glu
2530 2535 2540

Leu Arg Ser Ile Ile Lys Glu Met Pro Val Pro Lys Ala Asp Lys Lys
2545 2550 2555 2560

Leu Gly Asn Asp Ile Asp Thr Leu Leu Thr Asn Ala Gly Thr Gln Val
2565 2570 2575

Met Glu Ser Leu Asn Arg Arg Met Ala Gly Asp Gln Lys Ala Thr Asn
2580 2585 2590

Val Gln Asp Ser Ile Asp Ala Leu Ser Glu Thr Ile Met Ala Ala Ala
2595 2600 2605

Leu Lys Arg Glu Ser Phe Tyr Asp Ala Val Ala Thr Pro Thr Gly Asn
2610 2615 2620

Phe Ile Asp Arg Ala Asn Gln Tyr Val Thr Asp Ser Ile Glu Arg Leu
2625 2630 2635 2640

Ser Glu Thr Val Ile Glu Lys Ala Asp Lys Val Ile Ala Asn Pro Ser
2645 2650 2655

Asn Ile Ala Ala Lys Gly Val Ala His Leu Ala Lys Leu Thr Ala Ala
2660 2665 2670

Ile Ala Ser Glu Lys Gln Gly Glu Ile Val Ala Gln Gly Val Met Thr
2675 2680 2685

Ala Met Asn Gln Gly Lys Val Trp Gln Pro Phe His Asp Leu Val Asn
2690 2695 2700

Asp Ile Val Gly Arg Thr Lys Thr Asn Ala Asn Val Tyr Asp Leu Ile
2705 2710 2715 2720

Lys Leu Val Lys Ser Gln Ile Ser Gln Asp Arg Gln Gln Phe Arg Glu
2725 2730 2735

His Leu Pro Thr Val Ile Ala Gly Lys Phe Ser Arg Lys Leu Thr Asp

2740 2745 2750

Thr Glu Trp Ser Ala Met His Thr Gly Leu Gly Lys Thr Asp Leu Ala
2755 2760 2765

Val Leu Arg Glu Thr Met Ser Met Ala Glu Ile Arg Asp Leu Leu Ser
2770 2775 2780

Ser Ser Lys Lys Val Lys Asp Glu Ile Ser Thr Leu Glu Lys Glu Ile
2785 2790 2795 2800

Gln Asn Gln Ala Gly Arg Asn Trp Asn Leu Val Gln Lys Lys Ser Lys
2805 2810 2815

Gln Leu Ala Gln Tyr Met Ile Met Gly Glu Val Gly Asn Asn Leu Leu
2820 2825 2830

Arg Asn Ala His Ala Ile Ser Arg Leu Leu Gly Glu Arg Ile Thr Asn
2835 2840 2845

Gly Pro Val Ala Asp Val Ala Ala Ile Asp Lys Leu Ile Thr Leu Tyr
2850 2855 2860

Ser Leu Glu Leu Met Asn Lys Ser Asp Arg Asp Leu Leu Ser Glu Leu
2865 2870 2875 2880

Ala Gln Ser Glu Val Glu Gly Met Glu Phe Ser Ile Ala Tyr Met Val
2885 2890 2895

Gly Gln Arg Thr Glu Glu Met Arg Lys Ala Lys Gly Asp Asn Arg Thr
2900 2905 2910

Leu Leu Asn His Phe Lys Gly Tyr Ile Pro Val Glu Asn Gln Gln Gly
2915 2920 2925

Val Asn Leu Ile Ile Ala Asp Asp Lys Glu Phe Ala Lys Leu Asn Ser
2930 2935 2940

Gln Ser Phe Thr Arg Ile Gly Thr Tyr Gln Gly Ser Thr Gly Phe Arg
2945 2950 2955 2960

Thr Gly Ser Lys Gly Tyr Tyr Phe Ser Pro Val Ala Ala Arg Ala Pro
2965 2970 2975

Tyr Ser Gln Gly Ile Leu Gln Asn Val Arg Asn Thr Ala Gly Gly Val
2980 2985 2990

Asp Ile Gly Thr Gly Phe Thr Leu Gly Thr Met Val Ala Gly Arg Ile

2995 3000 3005

Thr Asp Lys Pro Thr Val Glu Arg Ile Thr Lys Ala Leu Ala Lys Gly
3010 3015 3020

Glu Arg Gly Arg Glu Pro Leu Met Pro Ile Tyr Asn Ser Lys Gly Gln
3025 3030 3035 3040

Val Val Ala Tyr Glu Gln Ser Val Asp Pro Asn Met Leu Lys His Leu
3045 3050 3055

Asn Gln Asp Asn His Phe Ala Lys Met Val Gly Val Trp Arg Gly Arg
3060 3065 3070

Gln Val Glu Glu Ala Lys Ala Gln Arg Phe Asn Asp Ile Leu Ile Glu
3075 3080 3085

Gln Leu His Ala Met Tyr Glu Lys Asp Ile Lys Asp Ser Ser Ala Asn
3090 3095 3100

Lys Ser Gln Tyr Val Asn Leu Leu Gly Lys Ile Asp Asp Pro Val Leu
3105 3110 3115 3120

Ala Asp Ala Ile Asn Leu Met Asn Ile Glu Thr Arg His Lys Ala Glu
3125 3130 3135

Glu Leu Phe Gly Lys Asp Glu Leu Trp Val Arg Arg Asp Met Leu Asn
3140 3145 3150

Asp Ala Leu Gly Tyr Arg Ala Ala Ser Ile Gly Asp Val Trp Thr Gly
3155 3160 3165

Asn Ser Arg Trp Ser Pro Ser Thr Leu Asp Thr Val Lys Lys Met Phe
3170 3175 3180

Leu Gly Ala Phe Gly Asn Lys Ala Tyr His Val Val Met Asn Ala Glu
3185 3190 3195 3200

Asn Thr Ile Gln Asn Leu Val Lys Asp Ala Lys Thr Val Ile Val Val
3205 3210 3215

Lys Ser Val Val Val Pro Ala Val Asn Phe Leu Ala Asn Ile Tyr Gln
3220 3225 3230

Met Ile Gly Arg Gly Val Pro Val Lys Asp Ile Ala Val Asn Ile Pro
3235 3240 3245

Arg Lys Thr Ser Glu Ile Asn Gln Tyr Ile Lys Ser Arg Leu Arg Gln

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   3250                3255                3260

Ile Asp Ala Glu Ala Glu Leu Arg Ala Ala Glu Gly Asn Pro Asn Leu
3265                3270                3275                3280

Val Arg Lys Leu Lys Thr Glu Ile Gln Ser Ile Thr Asp Ser His Arg
               3285                3290                3295

Arg Met Ser Ile Trp Pro Leu Ile Glu Ala Gly Glu Phe Ser Ser Ile
           3300                3305                3310

Ala Asp Ala Gly Ile Ser Arg Asp Asp Leu Leu Val Ala Glu Gly Lys
       3315                3320                3325

Ile His Glu Tyr Met Glu Lys Leu Ala Asn Lys Leu Pro Glu Lys Val
   3330                3335                3340

Arg Asn Ala Gly Arg Tyr Ala Leu Ile Ala Lys Asp Thr Ala Leu Phe
3345                3350                3355                3360

Gln Gly Ile Gln Lys Thr Val Glu Tyr Ser Asp Phe Ile Ala Lys Ala
               3365                3370                3375

Ile Ile Tyr Asp Asp Leu Val Lys Arg Lys Lys Lys Ser Ser Ser Glu
           3380                3385                3390

Ala Leu Gly Gln Val Thr Glu Glu Phe Ile Asn Tyr Asp Arg Leu Pro
       3395                3400                3405

Gly Arg Phe Arg Gly Tyr Met Glu Ser Met Gly Leu Met Trp Phe Tyr
   3410                3415                3420

Asn Phe Lys Ile Arg Ser Ile Lys Val Ala Met Ser Met Ile Arg Asn
3425                3430                3435                3440

Asn Pro Val His Ser Leu Ile Ala Thr Val Val Pro Ala Pro Thr Met
               3445                3450                3455

Phe Gly Asn Val Gly Leu Pro Ile Gln Asp Asn Met Leu Thr Met Leu
           3460                3465                3470

Ala Glu Gly Arg Leu Asp Tyr Ser Leu Gly Phe Gly Gln Gly Leu Arg
       3475                3480                3485

Ala Pro Thr Leu Asn Pro Trp Phe Asn Leu Thr His
   3490                3495                3500
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<210> 3
<211> 3318
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 3
gaaagtacag ttacagaaga attaaaagaa ggtattgatg ctgtttaccc ttcattggta 60

ggtactgctg attctaaagc agagggtatt aagaactatt tcaaattgtc ctttacctta 120

ccagaagaac agaaatcccg tactgttggt tcagaagcac ctctaaaaga tgtagcccaa 180

gctctgtctt ctcgtgctcg ttatgaactc tttactgaga aagaaactgc taaccctgct 240

tttaatgggg aagttattaa gcgatacaaa gaactcatgg aacatgggga aggtattgct 300

gatattcttc gctcccgtct ggctaagttc cttaacacta aggatgttgg taaacgtttt 360

gctcaaggta cagaagccaa ccgttgggta ggtggtaagt tacttaacat tgttgagcag 420

gatggggata cctttaagta caacgaacaa ttgctacaga ctgctgtatt agcaggtctt 480

caatggagac ttactgctac cagcaatact gctatcaaag atgcaaaaga tgttgctgct 540

attactggta ttgaccaagc tctgctgcca gaaggtttag tagagcaatt tgatactggt 600

atgacactca ctgaagcagt tagttccctg gctcagaaaa ttgagtctta ctggggatta 660

tctcgtaatc caaatgctcc attgggctat accaaaggca tccctacagc aatggctgct 720

gaaattctgg ctgcatttgt agagtctact gatgttgtag agaacatcgt ggatatgtca 780

gaaattgacc cagataacaa gaagactatt ggtctgtaca ccattactga actggattcc 840

ttcgacccaa ttaatagctt ccctactgct attgaagaag ctgttttagt gaatcctaca 900

gagaagatgt tctttggtga tgacattcct cctgtagcta atactcagct tcgtaaccct 960

gctgttcgta atactccaga acagaaggct gcattgaaag cagagcaggc tacagagttc 1020

tatgtacaca ccccaatggt tcaattctat gagacgttag gtaaagaccg tattctcgaa 1080

ctgatgggtg ctggtactct gaataaagag ttacttaatg ataaccatgc taaatctctg 1140

gaaggtaaga accgttcagt agaggactct tacaaccaac tgttctccgt cattgagcag 1200

gtaagagcac agagcgaaga catctctact gtacctattc actatgcata caatatgacc 1260

cgtgttggtc gtatgcagat gttaggtaaa tacaatcctc aatcagccaa actggttcgt 1320

gaggccatct tacctactaa agctactttg gatttatcga accagaacaa tgaagacttc 1380

tctgcattcc agttaggtct ggctcaggca ttggacatta aagtccatac tatgactcgt 1440

gaggttatgt ctgacgagtt gactaaatta ctggaaggta atctgaaacc agccattgat 1500

atgatggttg agtttaatac cactggttcc ttaccagaaa acgcagttga tgttctgaat 1560

acagcattag gagataggaa gtcattcgta gcattgatgg ctcttatgga gtattcccgt 1620

tacttagtag cagaggataa atctgcattt gtaactccac tgtatgtaga agcagatggt 1680

gttactaatg gtccaatcaa tgccatgatg ctaatgacag gcggtctgtt tactcctgac 1740

tggattcgta atattgccaa agggggcttg ttcattggtt ctccaaataa gaccatgaat 1800

gagcatcgct ctactgctga caataatgat ttatatcaag catccactaa tgctttgatg 1860

gaatcgttgg gtaagttacg tagtaactat gcctctaata tgcctattca gtctcagata 1920

gacagtcttc tttctctgat ggatttgttt ttaccggata ttaatcttgg tgagaatggt 1980

gctttagaac ttaaacgtgg tattgctaag aacccactga ctattaccat ctatggttct 2040

ggtgctcgtg gtattgcagg taagctggtt agttctgtta ctgatgccat ctatgagcgt 2100

atgtctgatg tactgaaagc tcgtgctaaa gacccaaata tctctgctgc tatggcaatg 2160

tttggtaagc aagctgcttc agaagcacat gctgaagaac ttcttgcccg tttcctgaaa 2220

gatatggaaa cactgacttc tactgttcct gttaaacgta aaggtgtact ggaactacaa 2280

tccacaggta caggagccaa aggaaaaatc aatcctaaga cctataccat taagggcgag 2340

caactgaagg cacttcagga aaatatgctg cacttctttg tagaaccact acgtaatggt 2400

attactcaga ctgtaggtga aagtctggtg tactctactg aacaattaca gaaagctact 2460

cagattcaat ctgtagtgct ggaagatatg ttcaaacagc gagtacaaga gaagctggca 2520

gagaaggcta aagacccaac atggaagaaa ggtgatttcc ttactcagaa agaactgaat 2580

gatattcagg cttctctgaa taacttagcc cctatgattg agactggttc tcagactttc 2640

tacattgctg gttcagaaaa tgcagaagta gcaaatcagg tattagctac taaccttgat 2700

gaccgtatgc gtgtaccaat gagtatctat gctccagcac aggccggtgt agcaggtatt 2760

ccatttatga ctattggtac tggtgatggc atgatgatgc aaactctttc cactatgaaa 2820

ggtgcaccaa agaataccct caaaatcttt gatggtatga acattggttt gaatgacatc 2880

actgatgcca gtcgtaaagc taatgaagct gtttacactt cttggcaggg taaccctatt 2940

aagaatgttt atgaatcata tgctaagttc atgaagaatg tagatttcag caagctgtcc 3000

cctgaagcat tggaagcaat tggtaaatct gctctggaat atgaccaacg tgagaatgct 3060

actgtagatg atattgctaa cgctgcatct ctgattgaac gtaacttacg taatattgca 3120

ctgggtgtag atattcgtca taaggtgctg gataaggtaa atctgtccat tgaccagatg 3180

gctgctgtag gtgctcctta tcagaacaac ggtaagattg acctcagcaa tatgacccct 3240

gaacaacagg ctgatgaact gaataaactt ttccgtgaag agttagaagc ccgtaaacaa 3300

aaagtcgcta aggctagg 3318

<210> 4
<211> 1107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 4

Met Glu Ser Thr Val Thr Glu Glu Leu Lys Glu Gly Ile Asp Ala Val
1 5 10 15

Tyr Pro Ser Leu Val Gly Thr Ala Asp Ser Lys Ala Glu Gly Ile Lys
20 25 30

Asn Tyr Phe Lys Leu Ser Phe Thr Leu Pro Glu Glu Gln Lys Ser Arg
35 40 45

Thr Val Gly Ser Glu Ala Pro Leu Lys Asp Val Ala Gln Ala Leu Ser

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     50                  55                  60

Ser Arg Ala Arg Tyr Glu Leu Phe Thr Glu Lys Glu Thr Ala Asn Pro
 65                  70                  75                  80

Ala Phe Asn Gly Glu Val Ile Lys Arg Tyr Lys Glu Leu Met Glu His
                 85                  90                  95

Gly Glu Gly Ile Ala Asp Ile Leu Arg Ser Arg Leu Ala Lys Phe Leu
            100                 105                 110

Asn Thr Lys Asp Val Gly Lys Arg Phe Ala Gln Gly Thr Glu Ala Asn
        115                 120                 125

Arg Trp Val Gly Gly Lys Leu Leu Asn Ile Val Glu Gln Asp Gly Asp
    130                 135                 140

Thr Phe Lys Tyr Asn Glu Gln Leu Leu Gln Thr Ala Val Leu Ala Gly
145                 150                 155                 160

Leu Gln Trp Arg Leu Thr Ala Thr Ser Asn Thr Ala Ile Lys Asp Ala
                165                 170                 175

Lys Asp Val Ala Ala Ile Thr Gly Ile Asp Gln Ala Leu Leu Pro Glu
            180                 185                 190

Gly Leu Val Glu Gln Phe Asp Thr Gly Met Thr Leu Thr Glu Ala Val
        195                 200                 205

Ser Ser Leu Ala Gln Lys Ile Glu Ser Tyr Trp Gly Leu Ser Arg Asn
    210                 215                 220

Pro Asn Ala Pro Leu Gly Tyr Thr Lys Gly Ile Pro Thr Ala Met Ala
225                 230                 235                 240

Ala Glu Ile Leu Ala Ala Phe Val Glu Ser Thr Asp Val Val Glu Asn
                245                 250                 255

Ile Val Asp Met Ser Glu Ile Asp Pro Asp Asn Lys Lys Thr Ile Gly
            260                 265                 270

Leu Tyr Thr Ile Thr Glu Leu Asp Ser Phe Asp Pro Ile Asn Ser Phe
        275                 280                 285

Pro Thr Ala Ile Glu Glu Ala Val Leu Val Asn Pro Thr Glu Lys Met
    290                 295                 300

Phe Phe Gly Asp Asp Ile Pro Pro Val Ala Asn Thr Gln Leu Arg Asn
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305 310 315 320

Pro Ala Val Arg Asn Thr Pro Glu Gln Lys Ala Ala Leu Lys Ala Glu
325 330 335

Gln Ala Thr Glu Phe Tyr Val His Thr Pro Met Val Gln Phe Tyr Glu
340 345 350

Thr Leu Gly Lys Asp Arg Ile Leu Glu Leu Met Gly Ala Gly Thr Leu
355 360 365

Asn Lys Glu Leu Leu Asn Asp Asn His Ala Lys Ser Leu Glu Gly Lys
370 375 380

Asn Arg Ser Val Glu Asp Ser Tyr Asn Gln Leu Phe Ser Val Ile Glu
385 390 395 400

Gln Val Arg Ala Gln Ser Glu Asp Ile Ser Thr Val Pro Ile His Tyr
405 410 415

Ala Tyr Asn Met Thr Arg Val Gly Arg Met Gln Met Leu Gly Lys Tyr
420 425 430

Asn Pro Gln Ser Ala Lys Leu Val Arg Glu Ala Ile Leu Pro Thr Lys
435 440 445

Ala Thr Leu Asp Leu Ser Asn Gln Asn Asn Glu Asp Phe Ser Ala Phe
450 455 460

Gln Leu Gly Leu Ala Gln Ala Leu Asp Ile Lys Val His Thr Met Thr
465 470 475 480

Arg Glu Val Met Ser Asp Glu Leu Thr Lys Leu Leu Glu Gly Asn Leu
485 490 495

Lys Pro Ala Ile Asp Met Met Val Glu Phe Asn Thr Thr Gly Ser Leu
500 505 510

Pro Glu Asn Ala Val Asp Val Leu Asn Thr Ala Leu Gly Asp Arg Lys
515 520 525

Ser Phe Val Ala Leu Met Ala Leu Met Glu Tyr Ser Arg Tyr Leu Val
530 535 540

Ala Glu Asp Lys Ser Ala Phe Val Thr Pro Leu Tyr Val Glu Ala Asp
545 550 555 560

Gly Val Thr Asn Gly Pro Ile Asn Ala Met Met Leu Met Thr Gly Gly

565 570 575

Leu Phe Thr Pro Asp Trp Ile Arg Asn Ile Ala Lys Gly Gly Leu Phe
580 585 590

Ile Gly Ser Pro Asn Lys Thr Met Asn Glu His Arg Ser Thr Ala Asp
595 600 605

Asn Asn Asp Leu Tyr Gln Ala Ser Thr Asn Ala Leu Met Glu Ser Leu
610 615 620

Gly Lys Leu Arg Ser Asn Tyr Ala Ser Asn Met Pro Ile Gln Ser Gln
625 630 635 640

Ile Asp Ser Leu Leu Ser Leu Met Asp Leu Phe Leu Pro Asp Ile Asn
645 650 655

Leu Gly Glu Asn Gly Ala Leu Glu Leu Lys Arg Gly Ile Ala Lys Asn
660 665 670

Pro Leu Thr Ile Thr Ile Tyr Gly Ser Gly Ala Arg Gly Ile Ala Gly
675 680 685

Lys Leu Val Ser Ser Val Thr Asp Ala Ile Tyr Glu Arg Met Ser Asp
690 695 700

Val Leu Lys Ala Arg Ala Lys Asp Pro Asn Ile Ser Ala Ala Met Ala
705 710 715 720

Met Phe Gly Lys Gln Ala Ala Ser Glu Ala His Ala Glu Glu Leu Leu
725 730 735

Ala Arg Phe Leu Lys Asp Met Glu Thr Leu Thr Ser Thr Val Pro Val
740 745 750

Lys Arg Lys Gly Val Leu Glu Leu Gln Ser Thr Gly Thr Gly Ala Lys
755 760 765

Gly Lys Ile Asn Pro Lys Thr Tyr Thr Ile Lys Gly Glu Gln Leu Lys
770 775 780

Ala Leu Gln Glu Asn Met Leu His Phe Phe Val Glu Pro Leu Arg Asn
785 790 795 800

Gly Ile Thr Gln Thr Val Gly Glu Ser Leu Val Tyr Ser Thr Glu Gln
805 810 815

Leu Gln Lys Ala Thr Gln Ile Gln Ser Val Val Leu Glu Asp Met Phe

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            820                 825                 830

Lys Gln Arg Val Gln Glu Lys Leu Ala Glu Lys Ala Lys Asp Pro Thr
        835                 840                 845

Trp Lys Lys Gly Asp Phe Leu Thr Gln Lys Glu Leu Asn Asp Ile Gln
    850                 855                 860

Ala Ser Leu Asn Asn Leu Ala Pro Met Ile Glu Thr Gly Ser Gln Thr
865                 870                 875                 880

Phe Tyr Ile Ala Gly Ser Glu Asn Ala Glu Val Ala Asn Gln Val Leu
                885                 890                 895

Ala Thr Asn Leu Asp Asp Arg Met Arg Val Pro Met Ser Ile Tyr Ala
            900                 905                 910

Pro Ala Gln Ala Gly Val Ala Gly Ile Pro Phe Met Thr Ile Gly Thr
        915                 920                 925

Gly Asp Gly Met Met Met Gln Thr Leu Ser Thr Met Lys Gly Ala Pro
    930                 935                 940

Lys Asn Thr Leu Lys Ile Phe Asp Gly Met Asn Ile Gly Leu Asn Asp
945                 950                 955                 960

Ile Thr Asp Ala Ser Arg Lys Ala Asn Glu Ala Val Tyr Thr Ser Trp
                965                 970                 975

Gln Gly Asn Pro Ile Lys Asn Val Tyr Glu Ser Tyr Ala Lys Phe Met
            980                 985                 990

Lys Asn Val Asp Phe Ser Lys Leu Ser Pro Glu Ala Leu Glu Ala Ile
        995                1000                1005

Gly Lys Ser Ala Leu Glu Tyr Asp Gln Arg Glu Asn Ala Thr Val Asp
   1010                1015                1020

Asp Ile Ala Asn Ala Ala Ser Leu Ile Glu Arg Asn Leu Arg Asn Ile
1025                1030                1035                1040

Ala Leu Gly Val Asp Ile Arg His Lys Val Leu Asp Lys Val Asn Leu
               1045                1050                1055

Ser Ile Asp Gln Met Ala Ala Val Gly Ala Pro Tyr Gln Asn Asn Gly
           1060                1065                1070

Lys Ile Asp Leu Ser Asn Met Thr Pro Glu Gln Gln Ala Asp Glu Leu
```

1075 1080 1085

Asn Lys Leu Phe Arg Glu Glu Leu Glu Ala Arg Lys Gln Lys Val Ala
1090 1095 1100

Lys Ala Arg
1105

<210> 5
<211> 3432
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 5
atgggggttt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa 60

atgggtcggg atctgtacga cgatgacgat aaggatccga gctcgagatc tgaaagtaca 120

gttacagaag aattaaaaga aggtattgat gctgtttacc cttcattggt aggtactgct 180

gattctaaag cagagggtat taagaactat ttcaaattgt cctttacctt accagaagaa 240

cagaaatccc gtactgttgg ttcagaagca cctctaaaag atgtagccca agctctgtct 300

tctcgtgctc gttatgaact ctttactgag aaagaaactg ctaaccctgc ttttaatggg 360

gaagttatta agcgatacaa agaactcatg gaacatgggg aaggtattgc tgatattctt 420

cgctcccgtc tggctaagtt ccttaacact aaggatgttg gtaaacgttt tgctcaaggt 480

acagaagcca accgttgggt aggtggtaag ttacttaaca ttgttgagca ggatggggat 540

acctttaagt acaacgaaca attgctacag actgctgtat tagcaggtct tcaatggaga 600

cttactgcta ccagcaatac tgctatcaaa gatgcaaaag atgttgctgc tattactggt 660

attgaccaag ctctgctgcc agaaggttta gtagagcaat ttgatactgg tatgacactc 720

actgaagcag ttagttccct ggctcagaaa attgagtctt actggggatt atctcgtaat 780

ccaaatgctc cattgggcta taccaaaggc atccctacag caatggctgc tgaaattctg 840

gctgcatttg tagagtctac tgatgttgta gagaacatcg tggatatgtc agaaattgac 900

ccagataaca agaagactat tggtctgtac accattactg aactggattc cttcgaccca 960

attaatagct tccctactgc tattgaagaa gctgttttag tgaatcctac agagaagatg 1020

ttctttggtg atgacattcc tcctgtagct aatactcagc ttcgtaaccc tgctgttcgt 1080

aatactccag aacagaaggc tgcattgaaa gcagagcagg ctacagagtt ctatgtacac 1140

accccaatgg ttcaattcta tgagacgtta ggtaaagacc gtattctcga actgatgggt 1200

gctggtactc tgaataaaga gttacttaat gataaccatg ctaaatctct ggaaggtaag 1260

aaccgttcag tagaggactc ttacaaccaa ctgttctccg tcattgagca ggtaagagca 1320

cagagcgaag acatctctac tgtacctatt cactatgcat acaatatgac ccgtgttggt 1380

cgtatgcaga tgttaggtaa atacaatcct caatcagcca aactggttcg tgaggccatc 1440

ttacctacta aagctacttt ggatttatcg aaccagaaca atgaagactt ctctgcattc 1500

cagttaggtc tggctcaggc attggacatt aaagtccata ctatgactcg tgaggttatg 1560

tctgacgagt tgactaaatt actggaaggt aatctgaaac cagccattga tatgatggtt 1620

gagtttaata ccactggttc cttaccagaa aacgcagttg atgttctgaa tacagcatta 1680

ggagatagga agtcattcgt agcattgatg gctcttatgg agtattcccg ttacttagta 1740

gcagaggata aatctgcatt tgtaactcca ctgtatgtag aagcagatgg tgttactaat 1800

ggtccaatca atgccatgat gctaatgaca ggcggtctgt ttactcctga ctggattcgt 1860

aatattgcca aaggggcctt gttcattggt tctccaaata agaccatgaa tgagcatcgc 1920

tctactgctg acaataatga tttatatcaa gcatccacta atgctttgat ggaatcgttg 1980

ggtaagttac gtagtaacta tgcctctaat atgcctattc agtctcagat agacagtctt 2040

ctttctctga tggatttgtt tttaccggat attaatcttg gtgagaatgg tgctttagaa 2100

cttaaacgtg gtattgctaa gaacccactg actattacca tctatggttc tggtgctcgt 2160

ggtattgcag gtaagctggt tagttctgtt actgatgcca tctatgagcg tatgtctgat 2220

gtactgaaag ctcgtgctaa agacccaaat atctctgctg ctatggcaat gtttggtaag 2280

caagctgctt cagaagcaca tgctgaagaa cttcttgccc gtttcctgaa agatatggaa 2340

acactgactt ctactgttcc tgttaaacgt aaaggtgtac tggaactaca atccacaggt 2400

acaggagcca aaggaaaaat caatcctaag acctatacca ttaagggcga gcaactgaag 2460

gcacttcagg aaaatatgct gcacttcttt gtagaaccac tacgtaatgg tattactcag 2520

actgtaggtg aaagtctggt gtactctact gaacaattac agaaagctac tcagattcaa 2580

tctgtagtgc tggaagatat gttcaaacag cgagtacaag agaagctggc agagaaggct 2640

aaagacccaa catggaagaa aggtgatttc cttactcaga aagaactgaa tgatattcag 2700

gcttctctga ataacttagc ccctatgatt gagactggtt ctcagacttt ctacattgct 2760

ggttcagaaa atgcagaagt agcaaatcag gtattagcta ctaaccttga tgaccgtatg 2820

cgtgtaccaa tgagtatcta tgctccagca caggccggtg tagcaggtat tccatttatg 2880

actattggta ctggtgatgg catgatgatg caaactcttt ccactatgaa aggtgcacca 2940

aagaataccc tcaaaatctt tgatggtatg aacattggtt tgaatgacat cactgatgcc 3000

agtcgtaaag ctaatgaagc tgtttacact tcttggcagg gtaaccctat taagaatgtt 3060

tatgaatcat atgctaagtt catgaagaat gtagatttca gcaagctgtc ccctgaagca 3120

ttggaagcaa ttggtaaatc tgctctggaa tatgaccaac gtgagaatgc tactgtagat 3180

gatattgcta acgctgcatc tctgattgaa cgtaacttac gtaatattgc actgggtgta 3240

gatattcgtc ataaggtgct ggataaggta aatctgtcca ttgaccagat ggctgctgta 3300

ggtgctcctt atcagaacaa cggtaagatt gacctcagca atatgacccc tgaacaacag 3360

gctgatgaac tgaataaact tttccgtgaa gagttagaag cccgtaaaca aaaagtcgct 3420

aaggctaggt aa 3432

<210> 6
<211> 1143
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Peptide

<400> 6

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Met Gly Gly Ser His His His His His His Gly Met Ala Ser Met Thr
  1               5                  10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
             20                  25                  30

Pro Ser Ser Arg Ser Glu Ser Thr Val Thr Glu Glu Leu Lys Glu Gly
         35                  40                  45

Ile Asp Ala Val Tyr Pro Ser Leu Val Gly Thr Ala Asp Ser Lys Ala
     50                  55                  60

Glu Gly Ile Lys Asn Tyr Phe Lys Leu Ser Phe Thr Leu Pro Glu Glu
 65                  70                  75                  80

Gln Lys Ser Arg Thr Val Gly Ser Glu Ala Pro Leu Lys Asp Val Ala
                 85                  90                  95

Gln Ala Leu Ser Ser Arg Ala Arg Tyr Glu Leu Phe Thr Glu Lys Glu
            100                 105                 110

Thr Ala Asn Pro Ala Phe Asn Gly Glu Val Ile Lys Arg Tyr Lys Glu
        115                 120                 125

Leu Met Glu His Gly Glu Gly Ile Ala Asp Ile Leu Arg Ser Arg Leu
    130                 135                 140

Ala Lys Phe Leu Asn Thr Lys Asp Val Gly Lys Arg Phe Ala Gln Gly
145                 150                 155                 160

Thr Glu Ala Asn Arg Trp Val Gly Gly Lys Leu Leu Asn Ile Val Glu
                165                 170                 175

Gln Asp Gly Asp Thr Phe Lys Tyr Asn Glu Gln Leu Leu Gln Thr Ala
            180                 185                 190

Val Leu Ala Gly Leu Gln Trp Arg Leu Thr Ala Thr Ser Asn Thr Ala
        195                 200                 205

Ile Lys Asp Ala Lys Asp Val Ala Ala Ile Thr Gly Ile Asp Gln Ala
    210                 215                 220

Leu Leu Pro Glu Gly Leu Val Glu Gln Phe Asp Thr Gly Met Thr Leu
225                 230                 235                 240
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Thr Glu Ala Val Ser Ser Leu Ala Gln Lys Ile Glu Ser Tyr Trp Gly
                245                 250                 255

Leu Ser Arg Asn Pro Asn Ala Pro Leu Gly Tyr Thr Lys Gly Ile Pro
            260                 265                 270

Thr Ala Met Ala Ala Glu Ile Leu Ala Ala Phe Val Glu Ser Thr Asp
        275                 280                 285

Val Val Glu Asn Ile Val Asp Met Ser Glu Ile Asp Pro Asp Asn Lys
    290                 295                 300

Lys Thr Ile Gly Leu Tyr Thr Ile Thr Glu Leu Asp Ser Phe Asp Pro
305                 310                 315                 320

Ile Asn Ser Phe Pro Thr Ala Ile Glu Glu Ala Val Leu Val Asn Pro
                325                 330                 335

Thr Glu Lys Met Phe Phe Gly Asp Asp Ile Pro Pro Val Ala Asn Thr
            340                 345                 350

Gln Leu Arg Asn Pro Ala Val Arg Asn Thr Pro Glu Gln Lys Ala Ala
        355                 360                 365

Leu Lys Ala Glu Gln Ala Thr Glu Phe Tyr Val His Thr Pro Met Val
    370                 375                 380

Gln Phe Tyr Glu Thr Leu Gly Lys Asp Arg Ile Leu Glu Leu Met Gly
385                 390                 395                 400

Ala Gly Thr Leu Asn Lys Glu Leu Leu Asn Asp Asn His Ala Lys Ser
                405                 410                 415

Leu Glu Gly Lys Asn Arg Ser Val Glu Asp Ser Tyr Asn Gln Leu Phe
            420                 425                 430

Ser Val Ile Glu Gln Val Arg Ala Gln Ser Glu Asp Ile Ser Thr Val
        435                 440                 445

Pro Ile His Tyr Ala Tyr Asn Met Thr Arg Val Gly Arg Met Gln Met
    450                 455                 460

Leu Gly Lys Tyr Asn Pro Gln Ser Ala Lys Leu Val Arg Glu Ala Ile
465                 470                 475                 480

Leu Pro Thr Lys Ala Thr Leu Asp Leu Ser Asn Gln Asn Asn Glu Asp
                485                 490                 495
```

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Phe Ser Ala Phe Gln Leu Gly Leu Ala Gln Ala Leu Asp Ile Lys Val
            500                 505                 510

His Thr Met Thr Arg Glu Val Met Ser Asp Glu Leu Thr Lys Leu Leu
        515                 520                 525

Glu Gly Asn Leu Lys Pro Ala Ile Asp Met Met Val Glu Phe Asn Thr
    530                 535                 540

Thr Gly Ser Leu Pro Glu Asn Ala Val Asp Val Leu Asn Thr Ala Leu
545                 550                 555                 560

Gly Asp Arg Lys Ser Phe Val Ala Leu Met Ala Leu Met Glu Tyr Ser
                565                 570                 575

Arg Tyr Leu Val Ala Glu Asp Lys Ser Ala Phe Val Thr Pro Leu Tyr
            580                 585                 590

Val Glu Ala Asp Gly Val Thr Asn Gly Pro Ile Asn Ala Met Met Leu
        595                 600                 605

Met Thr Gly Gly Leu Phe Thr Pro Asp Trp Ile Arg Asn Ile Ala Lys
    610                 615                 620

Gly Gly Leu Phe Ile Gly Ser Pro Asn Lys Thr Met Asn Glu His Arg
625                 630                 635                 640

Ser Thr Ala Asp Asn Asn Asp Leu Tyr Gln Ala Ser Thr Asn Ala Leu
                645                 650                 655

Met Glu Ser Leu Gly Lys Leu Arg Ser Asn Tyr Ala Ser Asn Met Pro
            660                 665                 670

Ile Gln Ser Gln Ile Asp Ser Leu Leu Ser Leu Met Asp Leu Phe Leu
        675                 680                 685

Pro Asp Ile Asn Leu Gly Glu Asn Gly Ala Leu Glu Leu Lys Arg Gly
    690                 695                 700

Ile Ala Lys Asn Pro Leu Thr Ile Thr Ile Tyr Gly Ser Gly Ala Arg
705                 710                 715                 720

Gly Ile Ala Gly Lys Leu Val Ser Ser Val Thr Asp Ala Ile Tyr Glu
                725                 730                 735

Arg Met Ser Asp Val Leu Lys Ala Arg Ala Lys Asp Pro Asn Ile Ser
            740                 745                 750
```

```
Ala Ala Met Ala Met Phe Gly Lys Gln Ala Ala Ser Glu Ala His Ala
        755                 760                 765

Glu Glu Leu Leu Ala Arg Phe Leu Lys Asp Met Glu Thr Leu Thr Ser
    770                 775                 780

Thr Val Pro Val Lys Arg Lys Gly Val Leu Glu Leu Gln Ser Thr Gly
785                 790                 795                 800

Thr Gly Ala Lys Gly Lys Ile Asn Pro Lys Thr Tyr Thr Ile Lys Gly
                805                 810                 815

Glu Gln Leu Lys Ala Leu Gln Glu Asn Met Leu His Phe Phe Val Glu
            820                 825                 830

Pro Leu Arg Asn Gly Ile Thr Gln Thr Val Gly Glu Ser Leu Val Tyr
        835                 840                 845

Ser Thr Glu Gln Leu Gln Lys Ala Thr Gln Ile Gln Ser Val Val Leu
    850                 855                 860

Glu Asp Met Phe Lys Gln Arg Val Gln Glu Lys Leu Ala Glu Lys Ala
865                 870                 875                 880

Lys Asp Pro Thr Trp Lys Lys Gly Asp Phe Leu Thr Gln Lys Glu Leu
                885                 890                 895

Asn Asp Ile Gln Ala Ser Leu Asn Asn Leu Ala Pro Met Ile Glu Thr
            900                 905                 910

Gly Ser Gln Thr Phe Tyr Ile Ala Gly Ser Glu Asn Ala Glu Val Ala
        915                 920                 925

Asn Gln Val Leu Ala Thr Asn Leu Asp Asp Arg Met Arg Val Pro Met
    930                 935                 940

Ser Ile Tyr Ala Pro Ala Gln Ala Gly Val Ala Gly Ile Pro Phe Met
945                 950                 955                 960

Thr Ile Gly Thr Gly Asp Gly Met Met Met Gln Thr Leu Ser Thr Met
                965                 970                 975

Lys Gly Ala Pro Lys Asn Thr Leu Lys Ile Phe Asp Gly Met Asn Ile
            980                 985                 990

Gly Leu Asn Asp Ile Thr Asp Ala Ser Arg Lys Ala Asn Glu Ala Val
        995                1000                1005
```

Tyr Thr Ser Trp Gln Gly Asn Pro Ile Lys Asn Val Tyr Glu Ser Tyr
1010 1015 1020

Ala Lys Phe Met Lys Asn Val Asp Phe Ser Lys Leu Ser Pro Glu Ala
1025 1030 1035 1040

Leu Glu Ala Ile Gly Lys Ser Ala Leu Glu Tyr Asp Gln Arg Glu Asn
1045 1050 1055

Ala Thr Val Asp Asp Ile Ala Asn Ala Ala Ser Leu Ile Glu Arg Asn
1060 1065 1070

Leu Arg Asn Ile Ala Leu Gly Val Asp Ile Arg His Lys Val Leu Asp
1075 1080 1085

Lys Val Asn Leu Ser Ile Asp Gln Met Ala Ala Val Gly Ala Pro Tyr
1090 1095 1100

Gln Asn Asn Gly Lys Ile Asp Leu Ser Asn Met Thr Pro Glu Gln Gln
1105 1110 1115 1120

Ala Asp Glu Leu Asn Lys Leu Phe Arg Glu Glu Leu Glu Ala Arg Lys
1125 1130 1135

Gln Lys Val Ala Lys Ala Arg
1140

<210> 7
<211> 3432
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 7
atgggggttt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa 60

atgggtcggg atctgtacga cgatgacgat aaggatccga gctcgagatc tgaaagtaca 120

gttacagaag aattaaaaga aggtattgat gctgtttacc cttcattggt aggtactgct 180

gattctaaag cagagggtat taagaactat ttcaaattgt cctttacctt accagaagaa 240

cagaaatccc gtactgttgg ttcagaagca cctctaaaag atgtagccca agctctgtct 300

tctcgtgctc gttatgaact ctttactgag aaagaaactg ctaaccctgc ttttaatggg 360

gaagttatta agcgatacaa agaactcatg gaacatgggg aaggtattgc tgatattctt 420

cgctcccgtc tggctaagtt ccttaacact aaggatgttg gtaaacgttt tgctcaaggt 480

acagaagcca accgttgggt aggtggtaag ttacttaaca ttgttgagca ggatggggat 540

acctttaagt acaacgaaca attgctacag actgctgtat tagcaggtct tcaatggaga 600

cttactgcta ccagcaatac tgctatcaaa gatgcaaaag atgttgctgc tattactggt 660

attgaccaag ctctgctgcc agaaggttta gtagagcaat ttgatactgg tatgacactc 720

actgaagcag ttagttccct ggctcagaaa attgagtctt actggggatt atctcgtaat 780

ccaaatgctc cattgggcta taccaaaggc atccctacag caatggctgc tgaaattctg 840

gctgcatttg tagagtctac tgatgttgta gagaacatcg tggatatgtc agaaattgac 900

ccagataaca agaagactat tggtctgtac accattactg aactggattc cttcgaccca 960

attaatagct tccctactgc tattgaagaa gctgttttag tgaatcctac agagaagatg 1020

ttctttggtg atgacattcc tcctgtagct aatactcagc ttcgtaaccc tgctgttcgt 1080

aatactccag aacagaaggc tgcattgaaa gcagagcagg ctacagagtt ctatgtacac 1140

accccaatgg ttcaattcta tgagacgtta ggtaaagacc gtattctcga actgatgggt 1200

gctggtactc tgaataaaga gttacttaat gataaccatg ctaaatctct ggaaggtaag 1260

aaccgttcag tagaggactc ttacaaccaa ctgttctccg tcattgagca ggtaagagca 1320

cagagcgaag acatctctac tgtacctatt cactatgcat acaatatgac ccgtgttggt 1380

cgtatgcaga tgttaggtaa atacaatcct caatcagcca aactggttcg tgaggccatc 1440

ttacctacta aagctacttt ggatttatcg aaccagaaca atgaagactt ctctgcattc 1500

cagttaggtc tggctcaggc attggacatt aaagtccata ctatgactcg tgaggttatg 1560

tctgacgagt tgactaaatt actggaaggt aatctgaaac cagccattga tatgatggtt 1620

gagtttaata ccactggttc cttaccagaa aacgcagttg atgttctgaa tacagcatta 1680

ggagatagga agtcattcgt agcattgatg gctcttatgg agtattcccg ttacttagta 1740

gcagaggata aatctgcatt tgtaactcca ctgtatgtag aagcagatgg tgttactaat 1800

ggtccaatca atgccatgat gctaatgaca ggcggtctgt ttactcctga ctggattcgt 1860

aatattgcca aaggggggctt gttcattggt tctccaaata agaccatgaa tgagcatcgc 1920

tctactgctg acaataatga tttatatcaa gcatccacta atgctttgat ggaatcgttg 1980

ggtaagttac gtagtaacta tgcctctaat atgcctattc agtctcagat agacagtctt 2040

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caagctgctt cagaagcaca tgctgaagaa cttcttgccc gtttcctgaa agatatggaa 2340

acactgactt ctactgttcc tgttaaacgt aaaggtgtac tggaactaca atccacaggt 2400

acaggagcca aaggaaaaat caatcctaag acctatacca ttaagggcga gcaactgaag 2460

gcacttcagg aaaatatgct gcacttcttt gtagaaccac tacgtaatgg tattactcag 2520

actgtaggtg aaagtctggt gtactctact gaacaattac agaaagctac tcagattcaa 2580

tctgtagtgc tggaagatat gttcaaacag cgagtacaag agaagctggc agagaaggct 2640

aaagacccaa catggaagaa aggtgatttc cttactcaga aagaactgaa tgatattcag 2700

gcttctctga ataacttagc ccctatgatt gagactggtt ctcagacttt ctacattgct 2760

ggttcagaaa atgcagaagt agcaaatcag gtattagcta ctaaccttga tgaccgtatg 2820

cgtgtaccaa tgagtatcta tgctccagca caggccggtg tagcaggtat tccatttatg 2880

actattggta ctggtgatgg catgatgatg caaactcttt ccactatgaa aggtgcacca 2940

aagaataccc tcaaaatctt tgatggtatg aacattggtt tgaatgacat cactgatgcc 3000

agtcgtaaag ctaatgaagc tgtttacact tcttggcagg gtaaccctat taagaatgtt 3060

tatgaatcat atgctaagtt catgaagaat gtagatttca gcaagctgtc ccctgaagca 3120

ttggaagcaa ttggtaaatc tgctctggaa tatgaccaac gtgagaatgc tactgtagat 3180

gatattgcta acgctgcatc tctgattgaa cgtaacttac gtaatattgc actgggtgta 3240

gatattcgtc ataaggtgct ggataaggta aatctgtcca ttgaccagat ggctgctgta 3300

ggtgctcctt atcagaacaa cggtaagatt gacctcagca atatgacccc tgaacaacag 3360

gctgatgaac tgaataaact tttccgtgaa gagttagaag cccgtaaaca aaaagtcgct 3420

aaggctaggt aa 3432

<210> 8
<211> 1143
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 8

Met Gly Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Pro Ser Ser Arg Ser Glu Ser Thr Val Thr Glu Glu Leu Lys Glu Gly
35 40 45

Ile Asp Ala Val Tyr Pro Ser Leu Val Gly Thr Ala Asp Ser Lys Ala
50 55 60

Glu Gly Ile Lys Asn Tyr Phe Lys Leu Ser Phe Thr Leu Pro Glu Glu
65 70 75 80

Gln Lys Ser Arg Thr Val Gly Ser Glu Ala Pro Leu Lys Asp Val Ala
85 90 95

Gln Ala Leu Ser Ser Arg Ala Arg Tyr Glu Leu Phe Thr Glu Lys Glu
100 105 110

Thr Ala Asn Pro Ala Phe Asn Gly Glu Val Ile Lys Arg Tyr Lys Glu
115 120 125

Leu Met Glu His Gly Glu Gly Ile Ala Asp Ile Leu Arg Ser Arg Leu
130 135 140

```
Ala Lys Phe Leu Asn Thr Lys Asp Val Gly Lys Arg Phe Ala Gln Gly
145                 150                 155                 160

Thr Glu Ala Asn Arg Trp Val Gly Gly Lys Leu Leu Asn Ile Val Glu
                165                 170                 175

Gln Asp Gly Asp Thr Phe Lys Tyr Asn Glu Gln Leu Leu Gln Thr Ala
            180                 185                 190

Val Leu Ala Gly Leu Gln Trp Arg Leu Thr Ala Thr Ser Asn Thr Ala
        195                 200                 205

Ile Lys Asp Ala Lys Asp Val Ala Ala Ile Thr Gly Ile Asp Gln Ala
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Leu Leu Pro Glu Gly Leu Val Glu Gln Phe Asp Thr Gly Met Thr Leu
225                 230                 235                 240

Thr Glu Ala Val Ser Ser Leu Ala Gln Lys Ile Glu Ser Tyr Trp Gly
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Leu Ser Arg Asn Pro Asn Ala Pro Leu Gly Tyr Thr Lys Gly Ile Pro
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Thr Ala Met Ala Ala Glu Ile Leu Ala Ala Phe Val Glu Ser Thr Asp
        275                 280                 285

Val Val Glu Asn Ile Val Asp Met Ser Glu Ile Asp Pro Asp Asn Lys
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Lys Thr Ile Gly Leu Tyr Thr Ile Thr Glu Leu Asp Ser Phe Asp Pro
305                 310                 315                 320

Ile Asn Ser Phe Pro Thr Ala Ile Glu Glu Ala Val Leu Val Asn Pro
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Thr Glu Lys Met Phe Phe Gly Asp Asp Ile Pro Pro Val Ala Asn Thr
            340                 345                 350

Gln Leu Arg Asn Pro Ala Val Arg Asn Thr Pro Glu Gln Lys Ala Ala
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Leu Lys Ala Glu Gln Ala Thr Glu Phe Tyr Val His Thr Pro Met Val
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Gln Phe Tyr Glu Thr Leu Gly Lys Asp Arg Ile Leu Glu Leu Met Gly
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Ala Gly Thr Leu Asn Lys Glu Leu Leu Asn Asp Asn His Ala Lys Ser
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Leu Glu Gly Lys Asn Arg Ser Val Glu Asp Ser Tyr Asn Gln Leu Phe
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Ser Val Ile Glu Gln Val Arg Ala Gln Ser Glu Asp Ile Ser Thr Val
        435                 440                 445

Pro Ile His Tyr Ala Tyr Asn Met Thr Arg Val Gly Arg Met Gln Met
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Leu Gly Lys Tyr Asn Pro Gln Ser Ala Lys Leu Val Arg Glu Ala Ile
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Leu Pro Thr Lys Ala Thr Leu Asp Leu Ser Asn Gln Asn Asn Glu Asp
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Phe Ser Ala Phe Gln Leu Gly Leu Ala Gln Ala Leu Asp Ile Lys Val
            500                 505                 510

His Thr Met Thr Arg Glu Val Met Ser Asp Glu Leu Thr Lys Leu Leu
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Glu Gly Asn Leu Lys Pro Ala Ile Asp Met Met Val Glu Phe Asn Thr
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Thr Gly Ser Leu Pro Glu Asn Ala Val Asp Val Leu Asn Thr Ala Leu
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Gly Asp Arg Lys Ser Phe Val Ala Leu Met Ala Leu Met Glu Tyr Ser
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Arg Tyr Leu Val Ala Glu Asp Lys Ser Ala Phe Val Thr Pro Leu Tyr
            580                 585                 590

Val Glu Ala Asp Gly Val Thr Asn Gly Pro Ile Asn Ala Met Met Leu
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Met Thr Gly Gly Leu Phe Thr Pro Asp Trp Ile Arg Asn Ile Ala Lys
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Gly Gly Leu Phe Ile Gly Ser Pro Asn Lys Thr Met Asn Glu His Arg
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Ser Thr Ala Asp Asn Asn Asp Leu Tyr Gln Ala Ser Thr Asn Ala Leu
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Met Glu Ser Leu Gly Lys Leu Arg Ser Asn Tyr Ala Ser Asn Met Pro
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Ile Gln Ser Gln Ile Asp Ser Leu Leu Ser Leu Met Asp Leu Phe Leu
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Pro Asp Ile Asn Leu Gly Glu Asn Gly Ala Leu Glu Leu Lys Arg Gly
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Ile Ala Lys Asn Pro Leu Thr Ile Thr Ile Phe Gly Ser Gly Ala Arg
705                 710                 715                 720

Gly Ile Ala Gly Lys Leu Val Ser Ser Val Thr Asp Ala Ile Tyr Glu
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Arg Met Ser Asp Val Leu Lys Ala Arg Ala Lys Asp Pro Asn Ile Ser
            740                 745                 750

Ala Ala Met Ala Met Phe Gly Lys Gln Ala Ala Ser Glu Ala His Ala
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Glu Glu Leu Leu Ala Arg Phe Leu Lys Asp Met Glu Thr Leu Thr Ser
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Thr Val Pro Val Lys Arg Lys Gly Val Leu Glu Leu Gln Ser Thr Gly
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Thr Gly Ala Lys Gly Lys Ile Asn Pro Lys Thr Tyr Thr Ile Lys Gly
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Glu Gln Leu Lys Ala Leu Gln Glu Asn Met Leu His Phe Phe Val Glu
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Pro Leu Arg Asn Gly Ile Thr Gln Thr Val Gly Glu Ser Leu Val Tyr
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Ser Thr Glu Gln Leu Gln Lys Ala Thr Gln Ile Gln Ser Val Val Leu
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Glu Asp Met Phe Lys Gln Arg Val Gln Glu Lys Leu Ala Glu Lys Ala
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Lys Asp Pro Thr Trp Lys Lys Gly Asp Phe Leu Thr Gln Lys Glu Leu
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Asn Asp Ile Gln Ala Ser Leu Asn Asn Leu Ala Pro Met Ile Glu Thr
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Ser Ile Tyr Ala Pro Ala Gln Ala Gly Val Ala Gly Ile Pro Phe Met
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Thr Ile Gly Thr Gly Asp Gly Met Met Met Gln Thr Leu Ser Thr Met
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Lys Gly Ala Pro Lys Asn Thr Leu Lys Ile Phe Asp Gly Met Asn Ile
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Gly Leu Asn Asp Ile Thr Asp Ala Ser Arg Lys Ala Asn Glu Ala Val
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Tyr Thr Ser Trp Gln Gly Asn Pro Ile Lys Asn Val Tyr Glu Ser Tyr
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Ala Lys Phe Met Lys Asn Val Asp Phe Ser Lys Leu Ser Pro Glu Ala
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Leu Glu Ala Ile Gly Lys Ser Ala Leu Glu Tyr Asp Gln Arg Glu Asn
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Ala Thr Val Asp Asp Ile Ala Asn Ala Ala Ser Leu Ile Glu Arg Asn
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Leu Arg Asn Ile Ala Leu Gly Val Asp Ile Arg His Lys Val Leu Asp
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Lys Val Asn Leu Ser Ile Asp Gln Met Ala Ala Val Gly Ala Pro Tyr
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Gln Asn Asn Gly Lys Ile Asp Leu Ser Asn Met Thr Pro Glu Gln Gln
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Ala Asp Glu Leu Asn Lys Leu Phe Arg Glu Glu Leu Glu Ala Arg Lys
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gatgtgtgga ccggtaactc tcgttggtca cctagcaccc ttgatactgt taagaagatg 9660

ttcctcggtg cattcggtaa taaggcatat catgtagtaa tgaatgctga aaataccatt 9720

cagaacttag tgaaggacgc taagacagta attgttgtta aatctgttgt agtaccggca 9780

gttaacttcc ttgctaacat ctaccagatg attggacgtg gtgttcctgt taaagatatt 9840

gctgtgaaca ttcctcgtaa gacgtcagag attaatcagt atattaaatc tcgtttacgt 9900

cagattgatg cggaagcaga gctacgtgct gctgaaggta accctaatct ggttcgtaaa 9960

cttaaaactg agattcaatc tattactgat agtcatcgtc gtatgagtat ctggcctttg 1002
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attgaagcag gtgagttctc ttctattgct gatgctggta ttagtcgtga tgacctgtta 1008
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gtagctgaag gtaagattca tgagtacatg gaaaaacttg ctaataaact tccagaaaaa 1014
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gtacgtaatg ctggccgtta cgctcttatt gctaaggaca ctgctctgtt ccagggtatc 1020
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cagaaaacag tagagtattc agactttatt gctaaagcca tcatctatga tgatttagtg 1026
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aaacgtaaga aaaaatcttc ttctgaagca ttaggtcagg taactgaaga gtttattaac 1032

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tatgacagat tgcctggtcg tttccgtggc tatatggaaa gtatgggtct gatgtggttc 1038
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tacaacttta aaattcgttc cattaaagtt gctatgagca tgattagaaa caacccagta 1044
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cattctctga ttgctacagt agtacctgct cctaccatgt ttggtaacgt aggtctacca 1050
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attcaggaca acatgctaac catgctggct gaaggaagac tggattactc attaggcttc 1056
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ggacaaggat taagagcacc taccctcaat ccttggttca accttactca ctaataa 1061
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<210> 15
<211> 3537
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 15
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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Pro Ser Ser Arg Ser Met Ser Val Phe Asp Arg Leu Ala Gly Phe Ala
35 40 45

Asp Ser Val Thr Asn Ala Lys Gln Val Asp Val Ser Thr Ala Thr Ala
50 55 60

Gln Lys Lys Ala Glu Gln Gly Val Thr Thr Pro Leu Val Ser Pro Asp
65 70 75 80

Ala Ala Tyr Gln Met Gln Ala Ala Arg Thr Gly Asn Val Gly Ala Asn
85 90 95

Ala Phe Glu Pro Gly Thr Val Gln Ser Asp Phe Met Asn Leu Thr Pro
100 105 110

Met Gln Ile Met Asn Lys Tyr Gly Val Glu Gln Gly Leu Gln Leu Ile
115 120 125

Asn Ala Arg Ala Asp Ala Gly Asn Gln Val Phe Asn Asp Ser Val Thr

130 135 140

Thr Arg Thr Pro Gly Glu Glu Leu Gly Asp Ile Ala Thr Gly Val Gly
145 150 155 160

Leu Gly Phe Val Asn Thr Leu Gly Gly Ile Gly Ala Leu Gly Ala Gly
165 170 175

Leu Leu Asn Asp Asp Ala Gly Ala Val Val Ala Gln Gln Leu Ser Lys
180 185 190

Phe Asn Asp Ala Val His Ala Thr Gln Ser Gln Ala Leu Gln Asp Lys
195 200 205

Arg Lys Leu Phe Ala Ala Arg Asn Leu Met Asn Glu Val Glu Ser Glu
210 215 220

Arg Gln Tyr Gln Thr Asp Lys Lys Glu Gly Thr Asn Asp Ile Val Ala
225 230 235 240

Ser Leu Ser Lys Phe Gly Arg Asp Phe Val Gly Ser Ile Glu Asn Ala
245 250 255

Ala Gln Thr Asp Ser Ile Ile Ser Asp Gly Leu Ala Glu Gly Val Gly
260 265 270

Ser Leu Leu Gly Ala Gly Pro Val Leu Arg Gly Ala Ser Leu Leu Gly
275 280 285

Lys Ala Val Val Pro Ala Asn Thr Leu Arg Ser Ala Ala Leu Ala Gly
290 295 300

Ala Ile Asp Ala Gly Thr Gly Thr Gln Ser Leu Ala Arg Ile Ala Ser
305 310 315 320

Thr Val Gly Arg Ala Ala Pro Gly Met Val Gly Val Gly Ala Met Glu
325 330 335

Ala Gly Gly Ala Tyr Gln Gln Thr Ala Asp Glu Ile Met Lys Met Ser
340 345 350

Leu Lys Asp Leu Glu Lys Ser Pro Val Tyr Gln Gln His Ile Lys Asp
355 360 365

Gly Met Ser Pro Glu Gln Ala Arg Arg Gln Thr Ala Ser Glu Thr Gly
370 375 380

Leu Thr Ala Ala Ala Ile Gln Leu Pro Ile Ala Ala Ala Thr Gly Pro

385 390 395 400

Leu Val Ser Arg Phe Glu Met Ala Pro Phe Arg Ala Gly Ser Leu Gly
405 410 415

Ala Val Gly Met Asn Leu Ala Arg Glu Thr Val Glu Glu Gly Val Gln
420 425 430

Gly Ala Thr Gly Gln Leu Ala Gln Asn Ile Ala Gln Gln Gln Asn Ile
435 440 445

Asp Lys Asn Gln Asp Leu Leu Lys Gly Val Gly Thr Gln Ala Gly Leu
450 455 460

Gly Ala Leu Tyr Gly Phe Gly Ser Ala Gly Val Val Gln Ala Pro Ala
465 470 475 480

Gly Ala Ala Arg Leu Ala Gly Ala Ala Thr Ala Pro Val Leu Arg Thr
485 490 495

Thr Met Ala Gly Val Lys Ala Ala Gly Ser Val Ala Gly Lys Val Val
500 505 510

Ser Pro Ile Lys Asn Thr Leu Val Ala Arg Gly Glu Arg Val Met Lys
515 520 525

Gln Asn Glu Glu Ala Ser Pro Val Ala Asp Asp Tyr Val Ala Gln Ala
530 535 540

Ala Gln Glu Ala Met Ala Gln Ala Pro Glu Ala Glu Val Thr Ile Arg
545 550 555 560

Asp Ala Val Glu Ala Thr Asp Ala Thr Pro Glu Gln Lys Val Ala Ala
565 570 575

His Gln Tyr Val Ser Asp Leu Met Asn Ala Thr Arg Phe Asn Pro Glu
580 585 590

Asn Tyr Gln Glu Ala Pro Glu His Ile Arg Asn Ala Val Ala Gly Ser
595 600 605

Thr Asp Gln Val Gln Val Ile Gln Lys Leu Ala Asp Leu Val Asn Thr
610 615 620

Leu Asp Glu Ser Asn Pro Gln Ala Leu Met Glu Ala Ala Ser Tyr Met
625 630 635 640

Tyr Asp Ala Val Ser Glu Phe Glu Gln Phe Ile Asn Arg Asp Pro Ala

645 650 655

Ala Leu Asp Ser Ile Pro Lys Asp Ser Pro Ala Ile Glu Leu Leu Asn
660 665 670

Arg Tyr Thr Asn Leu Thr Ala Asn Ile Gln Asn Thr Pro Lys Val Ile
675 680 685

Gly Ala Leu Asn Val Ile Asn Arg Met Ile Asn Glu Ser Ala Gln Asn
690 695 700

Gly Ser Leu Asn Val Thr Glu Glu Ser Ser Pro Gln Glu Met Gln Asn
705 710 715 720

Val Ala Leu Ala Ala Glu Val Ala Pro Glu Lys Leu Asn Pro Glu Ser
725 730 735

Val Asn Val Val Leu Lys His Ala Ala Asp Gly Arg Ile Lys Leu Asn
740 745 750

Asn Arg Gln Ile Ala Ala Leu Gln Asn Ala Ala Ala Ile Leu Lys Gly
755 760 765

Ala Arg Glu Tyr Asp Ala Glu Ala Ala Arg Leu Gly Leu Arg Pro Gln
770 775 780

Asp Ile Val Ser Lys Gln Ile Lys Thr Asp Glu Ser Arg Thr Gln Glu
785 790 795 800

Gly Gln Tyr Ser Ala Leu Gln His Ala Asn Arg Ile Arg Ser Ala Tyr
805 810 815

Asn Ser Gly Asn Phe Glu Leu Ala Ser Ala Tyr Leu Asn Asp Phe Met
820 825 830

Gln Phe Ala Gln His Met Gln Asn Lys Val Gly Ala Leu Asn Glu His
835 840 845

Leu Val Thr Gly Asn Ala Asp Lys Asn Lys Ser Val His Tyr Gln Ala
850 855 860

Leu Thr Ala Asp Arg Glu Trp Val Arg Ser Arg Thr Gly Leu Gly Val
865 870 875 880

Asn Pro Tyr Asp Thr Lys Ser Val Lys Phe Ala Gln Gln Val Ala Leu
885 890 895

Glu Ala Lys Thr Val Ala Asp Ile Ala Asn Ala Leu Ala Ser Ala Tyr

900 905 910

Pro Glu Leu Lys Val Ser His Ile Lys Val Thr Pro Leu Asp Ser Arg
915 920 925

Leu Asn Ala Pro Ala Ala Glu Val Val Lys Ala Phe Arg Gln Gly Asn
930 935 940

Arg Asp Val Ala Ser Ser Gln Pro Lys Ala Asp Ser Val Asn Gln Val
945 950 955 960

Lys Glu Thr Pro Val Thr Lys Gln Glu Pro Val Thr Ser Thr Val Gln
965 970 975

Thr Lys Thr Pro Val Ser Glu Ser Val Lys Thr Glu Pro Thr Thr Lys
980 985 990

Glu Ser Ser Pro Gln Ala Ile Lys Glu Pro Val Asn Gln Ser Glu Lys
995 1000 1005

Gln Asp Val Asn Leu Thr Asn Glu Asp Asn Ile Lys Gln Pro Thr Glu
1010 1015 1020

Ser Val Lys Glu Thr Glu Thr Ser Thr Lys Glu Ser Thr Val Thr Glu
1025 1030 1035 1040

Glu Leu Lys Glu Gly Ile Asp Ala Val Tyr Pro Ser Leu Val Gly Thr
1045 1050 1055

Ala Asp Ser Lys Ala Glu Gly Ile Lys Asn Tyr Phe Lys Leu Ser Phe
1060 1065 1070

Thr Leu Pro Glu Glu Gln Lys Ser Arg Thr Val Gly Ser Glu Ala Pro
1075 1080 1085

Leu Lys Asp Val Ala Gln Ala Leu Ser Ser Arg Ala Arg Tyr Glu Leu
1090 1095 1100

Phe Thr Glu Lys Glu Thr Ala Asn Pro Ala Phe Asn Gly Glu Val Ile
1105 1110 1115 1120

Lys Arg Tyr Lys Glu Leu Met Glu His Gly Glu Gly Ile Ala Asp Ile
1125 1130 1135

Leu Arg Ser Arg Leu Ala Lys Phe Leu Asn Thr Lys Asp Val Gly Lys
1140 1145 1150

Arg Phe Ala Gln Gly Thr Glu Ala Asn Arg Trp Val Gly Gly Lys Leu

1155 1160 1165

Leu Asn Ile Val Glu Gln Asp Gly Asp Thr Phe Lys Tyr Asn Glu Gln
1170 1175 1180

Leu Leu Gln Thr Ala Val Leu Ala Gly Leu Gln Trp Arg Leu Thr Ala
1185 1190 1195 1200

Thr Ser Asn Thr Ala Ile Lys Asp Ala Lys Asp Val Ala Ala Ile Thr
1205 1210 1215

Gly Ile Asp Gln Ala Leu Leu Pro Glu Gly Leu Val Glu Gln Phe Asp
1220 1225 1230

Thr Gly Met Thr Leu Thr Glu Ala Val Ser Ser Leu Ala Gln Lys Ile
1235 1240 1245

Glu Ser Tyr Trp Gly Leu Ser Arg Asn Pro Asn Ala Pro Leu Gly Tyr
1250 1255 1260

Thr Lys Gly Ile Pro Thr Ala Met Ala Ala Glu Ile Leu Ala Ala Phe
1265 1270 1275 1280

Val Glu Ser Thr Asp Val Val Glu Asn Ile Val Asp Met Ser Glu Ile
1285 1290 1295

Asp Pro Asp Asn Lys Lys Thr Ile Gly Leu Tyr Thr Ile Thr Glu Leu
1300 1305 1310

Asp Ser Phe Asp Pro Ile Asn Ser Phe Pro Thr Ala Ile Glu Glu Ala
1315 1320 1325

Val Leu Val Asn Pro Thr Glu Lys Met Phe Phe Gly Asp Asp Ile Pro
1330 1335 1340

Pro Val Ala Asn Thr Gln Leu Arg Asn Pro Ala Val Arg Asn Thr Pro
1345 1350 1355 1360

Glu Gln Lys Ala Ala Leu Lys Ala Glu Gln Ala Thr Glu Phe Tyr Val
1365 1370 1375

His Thr Pro Met Val Gln Phe Tyr Glu Thr Leu Gly Lys Asp Arg Ile
1380 1385 1390

Leu Glu Leu Met Gly Ala Gly Thr Leu Asn Lys Glu Leu Leu Asn Asp
1395 1400 1405

Asn His Ala Lys Ser Leu Glu Gly Lys Asn Arg Ser Val Glu Asp Ser

1410 1415 1420

Tyr Asn Gln Leu Phe Ser Val Ile Glu Gln Val Arg Ala Gln Ser Glu
1425 1430 1435 1440

Asp Ile Ser Thr Val Pro Ile His Tyr Ala Tyr Asn Met Thr Arg Val
1445 1450 1455

Gly Arg Met Gln Met Leu Gly Lys Tyr Asn Pro Gln Ser Ala Lys Leu
1460 1465 1470

Val Arg Glu Ala Ile Leu Pro Thr Lys Ala Thr Leu Asp Leu Ser Asn
1475 1480 1485

Gln Asn Asn Glu Asp Phe Ser Ala Phe Gln Leu Gly Leu Ala Gln Ala
1490 1495 1500

Leu Asp Ile Lys Val His Thr Met Thr Arg Glu Val Met Ser Asp Glu
1505 1510 1515 1520

Leu Thr Lys Leu Leu Glu Gly Asn Leu Lys Pro Ala Ile Asp Met Met
1525 1530 1535

Val Glu Phe Asn Thr Thr Gly Ser Leu Pro Glu Asn Ala Val Asp Val
1540 1545 1550

Leu Asn Thr Ala Leu Gly Asp Arg Lys Ser Phe Val Ala Leu Met Ala
1555 1560 1565

Leu Met Glu Tyr Ser Arg Tyr Leu Val Ala Glu Asp Lys Ser Ala Phe
1570 1575 1580

Val Thr Pro Leu Tyr Val Glu Ala Asp Gly Val Thr Asn Gly Pro Ile
1585 1590 1595 1600

Asn Ala Met Met Leu Met Thr Gly Gly Leu Phe Thr Pro Asp Trp Ile
1605 1610 1615

Arg Asn Ile Ala Lys Gly Gly Leu Phe Ile Gly Ser Pro Asn Lys Thr
1620 1625 1630

Met Asn Glu His Arg Ser Thr Ala Asp Asn Asn Asp Leu Tyr Gln Ala
1635 1640 1645

Ser Thr Asn Ala Leu Met Glu Ser Leu Gly Lys Leu Arg Ser Asn Tyr
1650 1655 1660

Ala Ser Asn Met Pro Ile Gln Ser Gln Ile Asp Ser Leu Leu Ser Leu

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1665                1670                1675                1680

Met Asp Leu Phe Leu Pro Asp Ile Asn Leu Gly Glu Asn Gly Ala Leu
                1685                1690                1695

Glu Leu Lys Arg Gly Ile Ala Lys Asn Pro Leu Thr Ile Thr Ile Tyr
            1700                1705                1710

Gly Ser Gly Ala Arg Gly Ile Ala Gly Lys Leu Val Ser Ser Val Thr
        1715                1720                1725

Asp Ala Ile Tyr Glu Arg Met Ser Asp Val Leu Lys Ala Arg Ala Lys
    1730                1735                1740

Asp Pro Asn Ile Ser Ala Ala Met Ala Met Phe Gly Lys Gln Ala Ala
1745                1750                1755                1760

Ser Glu Ala His Ala Glu Glu Leu Leu Ala Arg Phe Leu Lys Asp Met
                1765                1770                1775

Glu Thr Leu Thr Ser Thr Val Pro Val Lys Arg Lys Gly Val Leu Glu
            1780                1785                1790

Leu Gln Ser Thr Gly Thr Gly Ala Lys Gly Lys Ile Asn Pro Lys Thr
        1795                1800                1805

Tyr Thr Ile Lys Gly Glu Gln Leu Lys Ala Leu Gln Glu Asn Met Leu
    1810                1815                1820

His Phe Phe Val Glu Pro Leu Arg Asn Gly Ile Thr Gln Thr Val Gly
1825                1830                1835                1840

Glu Ser Leu Val Tyr Ser Thr Glu Gln Leu Gln Lys Ala Thr Gln Ile
                1845                1850                1855

Gln Ser Val Val Leu Glu Asp Met Phe Lys Gln Arg Val Gln Glu Lys
            1860                1865                1870

Leu Ala Glu Lys Ala Lys Asp Pro Thr Trp Lys Lys Gly Asp Phe Leu
        1875                1880                1885

Thr Gln Lys Glu Leu Asn Asp Ile Gln Ala Ser Leu Asn Asn Leu Ala
    1890                1895                1900

Pro Met Ile Glu Thr Gly Ser Gln Thr Phe Tyr Ile Ala Gly Ser Glu
1905                1910                1915                1920

Asn Ala Glu Val Ala Asn Gln Val Leu Ala Thr Asn Leu Asp Asp Arg
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1925 1930 1935

Met Arg Val Pro Met Ser Ile Tyr Ala Pro Ala Gln Ala Gly Val Ala
1940 1945 1950

Gly Ile Pro Phe Met Thr Ile Gly Thr Gly Asp Gly Met Met Met Gln
1955 1960 1965

Thr Leu Ser Thr Met Lys Gly Ala Pro Lys Asn Thr Leu Lys Ile Phe
1970 1975 1980

Asp Gly Met Asn Ile Gly Leu Asn Asp Ile Thr Asp Ala Ser Arg Lys
1985 1990 1995 2000

Ala Asn Glu Ala Val Tyr Thr Ser Trp Gln Gly Asn Pro Ile Lys Asn
2005 2010 2015

Val Tyr Glu Ser Tyr Ala Lys Phe Met Lys Asn Val Asp Phe Ser Lys
2020 2025 2030

Leu Ser Pro Glu Ala Leu Glu Ala Ile Gly Lys Ser Ala Leu Glu Tyr
2035 2040 2045

Asp Gln Arg Glu Asn Ala Thr Val Asp Asp Ile Ala Asn Ala Ala Ser
2050 2055 2060

Leu Ile Glu Arg Asn Leu Arg Asn Ile Ala Leu Gly Val Asp Ile Arg
2065 2070 2075 2080

His Lys Val Leu Asp Lys Val Asn Leu Ser Ile Asp Gln Met Ala Ala
2085 2090 2095

Val Gly Ala Pro Tyr Gln Asn Asn Gly Lys Ile Asp Leu Ser Asn Met
2100 2105 2110

Thr Pro Glu Gln Gln Ala Asp Glu Leu Asn Lys Leu Phe Arg Glu Glu
2115 2120 2125

Leu Glu Ala Arg Lys Gln Lys Val Ala Lys Ala Arg Ala Glu Val Lys
2130 2135 2140

Glu Glu Thr Val Ser Glu Lys Glu Pro Val Asn Pro Asp Phe Gly Met
2145 2150 2155 2160

Val Gly Arg Glu His Lys Ala Ser Gly Val Arg Ile Leu Ser Ala Thr
2165 2170 2175

Ala Ile Arg Asn Leu Ala Lys Ile Ser Asn Leu Pro Ser Thr Gln Ala

2180 2185 2190

Ala Thr Leu Ala Glu Ile Gln Lys Ser Leu Ala Ala Lys Asp Tyr Lys
2195 2200 2205

Ile Ile Tyr Gly Thr Pro Thr Gln Val Ala Glu Tyr Ala Arg Gln Lys
2210 2215 2220

Asn Val Thr Glu Leu Thr Ser Gln Glu Met Glu Glu Ala Gln Ala Gly
2225 2230 2235 2240

Asn Ile Tyr Gly Trp Thr Asn Phe Asp Asp Lys Thr Ile Tyr Leu Val
2245 2250 2255

Ser Pro Ser Met Glu Thr Leu Ile His Glu Leu Val His Ala Ser Thr
2260 2265 2270

Phe Glu Glu Val Tyr Ser Phe Tyr Gln Gly Asn Glu Val Ser Pro Thr
2275 2280 2285

Ser Lys Gln Ala Ile Glu Asn Leu Glu Gly Leu Met Glu Gln Phe Arg
2290 2295 2300

Ser Leu Asp Ile Ser Lys Asp Ser Pro Glu Met Arg Glu Ala Tyr Ala
2305 2310 2315 2320

Asp Ala Ile Ala Thr Ile Glu Gly His Leu Ser Asn Gly Phe Val Asp
2325 2330 2335

Pro Ala Ile Ser Lys Ala Ala Ala Leu Asn Glu Phe Met Ala Trp Gly
2340 2345 2350

Leu Ala Asn Arg Ala Leu Ala Ala Lys Gln Lys Arg Thr Ser Ser Leu
2355 2360 2365

Val Gln Met Val Lys Asp Val Tyr Gln Ala Ile Lys Lys Leu Ile Trp
2370 2375 2380

Gly Arg Lys Gln Ala Pro Ala Leu Gly Glu Asp Met Phe Ser Asn Leu
2385 2390 2395 2400

Leu Phe Asn Ser Ala Ile Leu Met Arg Ser Gln Pro Thr Thr Gln Ala
2405 2410 2415

Val Ala Lys Asp Gly Thr Leu Phe His Ser Lys Ala Tyr Gly Asn Asn
2420 2425 2430

Glu Arg Leu Ser Gln Leu Asn Gln Thr Phe Asp Lys Leu Val Thr Asp

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      2435                2440                2445

Tyr Leu Arg Thr Asp Pro Val Thr Glu Val Glu Arg Arg Gly Asn Val
   2450                2455                2460

Ala Asn Ala Leu Met Ser Ala Thr Arg Leu Val Arg Asp Val Gln Ser
2465                2470                2475                2480

His Gly Phe Asn Met Thr Ala Gln Glu Gln Ser Val Phe Gln Met Val
               2485                2490                2495

Thr Ala Ala Leu Ala Thr Glu Ala Ala Ile Asp Pro His Ala Met Ala
          2500                2505                2510

Arg Ala Gln Glu Leu Tyr Thr His Val Met Lys His Leu Thr Val Glu
      2515                2520                2525

His Phe Met Ala Asp Pro Asp Ser Thr Asn Pro Ala Asp Arg Tyr Tyr
   2530                2535                2540

Ala Gln Gln Lys Tyr Asp Thr Ile Ser Gly Ala Asn Leu Val Glu Val
2545                2550                2555                2560

Asp Ala Lys Gly Arg Thr Ser Leu Leu Pro Thr Phe Leu Gly Leu Ala
               2565                2570                2575

Met Val Asn Glu Glu Leu Arg Ser Ile Ile Lys Glu Met Pro Val Pro
          2580                2585                2590

Lys Ala Asp Lys Lys Leu Gly Asn Asp Ile Asp Thr Leu Leu Thr Asn
      2595                2600                2605

Ala Gly Thr Gln Val Met Glu Ser Leu Asn Arg Arg Met Ala Gly Asp
   2610                2615                2620

Gln Lys Ala Thr Asn Val Gln Asp Ser Ile Asp Ala Leu Ser Glu Thr
2625                2630                2635                2640

Ile Met Ala Ala Ala Leu Lys Arg Glu Ser Phe Tyr Asp Ala Val Ala
               2645                2650                2655

Thr Pro Thr Gly Asn Phe Ile Asp Arg Ala Asn Gln Tyr Val Thr Asp
          2660                2665                2670

Ser Ile Glu Arg Leu Ser Glu Thr Val Ile Glu Lys Ala Asp Lys Val
      2675                2680                2685

Ile Ala Asn Pro Ser Asn Ile Ala Ala Lys Gly Val Ala His Leu Ala
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2690 2695 2700

Lys Leu Thr Ala Ala Ile Ala Ser Glu Lys Gln Gly Glu Ile Val Ala
2705 2710 2715 2720

Gln Gly Val Met Thr Ala Met Asn Gln Gly Lys Val Trp Gln Pro Phe
2725 2730 2735

His Asp Leu Val Asn Asp Ile Val Gly Arg Thr Lys Thr Asn Ala Asn
2740 2745 2750

Val Tyr Asp Leu Ile Lys Leu Val Lys Ser Gln Ile Ser Gln Asp Arg
2755 2760 2765

Gln Gln Phe Arg Glu His Leu Pro Thr Val Ile Ala Gly Lys Phe Ser
2770 2775 2780

Arg Lys Leu Thr Asp Thr Glu Trp Ser Ala Met His Thr Gly Leu Gly
2785 2790 2795 2800

Lys Thr Asp Leu Ala Val Leu Arg Glu Thr Met Ser Met Ala Glu Ile
2805 2810 2815

Arg Asp Leu Leu Ser Ser Ser Lys Lys Val Lys Asp Glu Ile Ser Thr
2820 2825 2830

Leu Glu Lys Glu Ile Gln Asn Gln Ala Gly Arg Asn Trp Asn Leu Val
2835 2840 2845

Gln Lys Lys Ser Lys Gln Leu Ala Gln Tyr Met Ile Met Gly Glu Val
2850 2855 2860

Gly Asn Asn Leu Leu Arg Asn Ala His Ala Ile Ser Arg Leu Leu Gly
2865 2870 2875 2880

Glu Arg Ile Thr Asn Gly Pro Val Ala Asp Val Ala Ala Ile Asp Lys
2885 2890 2895

Leu Ile Thr Leu Tyr Ser Leu Glu Leu Met Asn Lys Ser Asp Arg Asp
2900 2905 2910

Leu Leu Ser Glu Leu Ala Gln Ser Glu Val Glu Gly Met Glu Phe Ser
2915 2920 2925

Ile Ala Tyr Met Val Gly Gln Arg Thr Glu Glu Met Arg Lys Ala Lys
2930 2935 2940

Gly Asp Asn Arg Thr Leu Leu Asn His Phe Lys Gly Tyr Ile Pro Val

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2945                2950                2955                2960

Glu Asn Gln Gln Gly Val Asn Leu Ile Ile Ala Asp Asp Lys Glu Phe
                2965                2970                2975

Ala Lys Leu Asn Ser Gln Ser Phe Thr Arg Ile Gly Thr Tyr Gln Gly
            2980                2985                2990

Ser Thr Gly Phe Arg Thr Gly Ser Lys Gly Tyr Tyr Phe Ser Pro Val
        2995                3000                3005

Ala Ala Arg Ala Pro Tyr Ser Gln Gly Ile Leu Gln Asn Val Arg Asn
    3010                3015                3020

Thr Ala Gly Gly Val Asp Ile Gly Thr Gly Phe Thr Leu Gly Thr Met
3025                3030                3035                3040

Val Ala Gly Arg Ile Thr Asp Lys Pro Thr Val Glu Arg Ile Thr Lys
                3045                3050                3055

Ala Leu Ala Lys Gly Glu Arg Gly Arg Glu Pro Leu Met Pro Ile Tyr
            3060                3065                3070

Asn Ser Lys Gly Gln Val Val Ala Tyr Glu Gln Ser Val Asp Pro Asn
        3075                3080                3085

Met Leu Lys His Leu Asn Gln Asp Asn His Phe Ala Lys Met Val Gly
    3090                3095                3100

Val Trp Arg Gly Arg Gln Val Glu Glu Ala Lys Ala Gln Arg Phe Asn
3105                3110                3115                3120

Asp Ile Leu Ile Glu Gln Leu His Ala Met Tyr Glu Lys Asp Ile Lys
                3125                3130                3135

Asp Ser Ser Ala Asn Lys Ser Gln Tyr Val Asn Leu Leu Gly Lys Ile
            3140                3145                3150

Asp Asp Pro Val Leu Ala Asp Ala Ile Asn Leu Met Asn Ile Glu Thr
        3155                3160                3165

Arg His Lys Ala Glu Glu Leu Phe Gly Lys Asp Glu Leu Trp Val Arg
    3170                3175                3180

Arg Asp Met Leu Asn Asp Ala Leu Gly Tyr Arg Ala Ala Ser Ile Gly
3185                3190                3195                3200

Asp Val Trp Thr Gly Asn Ser Arg Trp Ser Pro Ser Thr Leu Asp Thr
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                3205                3210                3215

Val Lys Lys Met Phe Leu Gly Ala Phe Gly Asn Lys Ala Tyr His Val
          3220                3225                3230

Val Met Asn Ala Glu Asn Thr Ile Gln Asn Leu Val Lys Asp Ala Lys
       3235                3240                3245

Thr Val Ile Val Val Lys Ser Val Val Val Pro Ala Val Asn Phe Leu
   3250                3255                3260

Ala Asn Ile Tyr Gln Met Ile Gly Arg Gly Val Pro Val Lys Asp Ile
3265                3270                3275                3280

Ala Val Asn Ile Pro Arg Lys Thr Ser Glu Ile Asn Gln Tyr Ile Lys
               3285                3290                3295

Ser Arg Leu Arg Gln Ile Asp Ala Glu Ala Glu Leu Arg Ala Ala Glu
          3300                3305                3310

Gly Asn Pro Asn Leu Val Arg Lys Leu Lys Thr Glu Ile Gln Ser Ile
       3315                3320                3325

Thr Asp Ser His Arg Arg Met Ser Ile Trp Pro Leu Ile Glu Ala Gly
   3330                3335                3340

Glu Phe Ser Ser Ile Ala Asp Ala Gly Ile Ser Arg Asp Asp Leu Leu
3345                3350                3355                3360

Val Ala Glu Gly Lys Ile His Glu Tyr Met Glu Lys Leu Ala Asn Lys
               3365                3370                3375

Leu Pro Glu Lys Val Arg Asn Ala Gly Arg Tyr Ala Leu Ile Ala Lys
          3380                3385                3390

Asp Thr Ala Leu Phe Gln Gly Ile Gln Lys Thr Val Glu Tyr Ser Asp
       3395                3400                3405

Phe Ile Ala Lys Ala Ile Ile Tyr Asp Asp Leu Val Lys Arg Lys Lys
   3410                3415                3420

Lys Ser Ser Ser Glu Ala Leu Gly Gln Val Thr Glu Glu Phe Ile Asn
3425                3430                3435                3440

Tyr Asp Arg Leu Pro Gly Arg Phe Arg Gly Tyr Met Glu Ser Met Gly
               3445                3450                3455

Leu Met Trp Phe Tyr Asn Phe Lys Ile Arg Ser Ile Lys Val Ala Met
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3460 3465 3470

Ser Met Ile Arg Asn Asn Pro Val His Ser Leu Ile Ala Thr Val Val
3475 3480 3485

Pro Ala Pro Thr Met Phe Gly Asn Val Gly Leu Pro Ile Gln Asp Asn
3490 3495 3500

Met Leu Thr Met Leu Ala Glu Gly Arg Leu Asp Tyr Ser Leu Gly Phe
3505 3510 3515 3520

Gly Gln Gly Leu Arg Ala Pro Thr Leu Asn Pro Trp Phe Asn Leu Thr
3525 3530 3535

His

<210> 16
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 16
ggcattactt catccaaaag aagcggagct tc 32

<210> 17
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 17
ggccatccat tacttcatcc aaaagaagcg gagcttc 37

<210> 18
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 18
ggatccaaaa gaagcggagc ttc 23

<210> 19
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 19
ggcattactt catccaaaag aagctgagct tc 32

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 20
ggcattactt catccaaaag aagcggagc 29

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 21
ggaggctcct cggagtctcc tttt 24

<210> 22
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 22
ggactacctt cgggtagtcc ttttt 25

<210> 23
<211> 33
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic Primer

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